

GenCore version 5.1.5  
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OM nucleic - nucleic search, using sw model

Run on: June 1, 2003, 15:19:59 ; Search time 5588.75 Seconds  
(without alignments)  
11622.905 Million cell updates/sec

Title: US-09-625-573-1  
Perfect score: 2232  
Sequence: 1 GGATTGAACAGGACGCATT.....TATAACTATGTGTGATAAAG 2232

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_htg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

15: em\_ba.\*

16: em\_fun.\*

17: em\_hum.\*

18: em\_in.\*

19: em\_mu.\*

20: em\_om.\*

21: em\_or.\*

22: em\_ov.\*

23: em\_pat.\*

24: em\_ph.\*

25: em\_pl.\*

26: em\_ro.\*

27: em\_sts.\*

28: em\_un.\*

29: em\_vi.\*

30: em\_htg\_hum.\*

31: em\_htg\_inv.\*

32: em\_htg\_other.\*

33: em\_htg\_mus.\*

34: em\_htg\_pln.\*

35: em\_htg\_rod.\*

36: em\_htg\_man.\*

37: em\_htg\_vrt.\*

38: em\_sy.\*

39: em\_htgo\_hum.\*

40: em\_htgo\_mus.\*

41: em\_htgo\_other.\*

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2232	100.0	2232	6	AR116074	AR116074 Sequence
2	2232	100.0	2232	6	I79542	I79542 Sequence 1
3	2232	100.0	2232	6	HSU03882	U03882 Human monoc
4	1254	56.2	5471	9	HSMPA02	U0924 Human monoc
5	1250.8	56.0	143068	6	AX335952	AX335952 Sequence
6	1250.8	56.0	143068	9	HSU95626	U95626 Homo sapien
7	1249.2	56.0	185437	9	AC098613	AC098613 Homo sapi
8	1068	47.8	1068	11	G07239	G07239 human STS W
9	980	43.9	1979	6	AR116075	AR116075 Sequence
10	980	43.9	1979	6	I79543	I79543 Sequence 3
11	980	43.9	1979	9	HSU03905	U03905 Human monoc
12	941	42.2	1083	6	AX232508	AX232508 Sequence
13	939.4	42.1	1083	6	AX232506	AX232506 Sequence
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18	816.6	36.6	2900	2	AC087602	AC087602 Pan trogl
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45	640.4	28.7	1019	9	AF162041	AF162041 Cercopith

ALIGNMENTS

RESULT 1  
AR116074  
LOCUS 2232 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 1 from patent US 6132987.  
ACCESSION AR116074  
VERSION AR116074.1 GI:14096396  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2232)  
AUTHORS Charo, I.F. and Coughlin, S.R.  
TITLE Recombinant mammalian monocyte chemotactic protein-1 (MCP-1)  
receptors (MCP-1R, CCR-2)  
JOURNAL Patent: US 6132987-A 1 17-OCT-2000;

FEATURES		Location/Qualifiers
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RESULT 3
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LOCUS Human monocyte chemoattractant protein 1 receptor (MCP-1RA)
DEFINITION alternatively spliced mRNA, complete cds.
ACCESSION U03882
VERSION U03882.1 GI:472555
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2232)
AUTHORS Charo, I.F., Myers, S.J., Herman, A., Franci, C., Connolly, A.J. and
Coughlin, S.R.
TITLE Molecular cloning and functional expression of two monocyte
chemoattractant protein 1 receptors reveals alternative splicing of
the carboxyl-terminal tails
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)
MEDLINE 94195821
PUBMED 8146186
REFERENCE 2 (bases 1 to 2232)
AUTHORS Myers, S.J.
TITLE Direct Submission
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JOURNAL Submitted (01-DEC-1993) Scott J. Myers, Cardiovascular, The
Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110,
USA
FEATURES
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RESULT 4  
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 Human monocyte chemoattractant protein 1 receptor gene, two  
 alternatively spliced forms, complete cds.  
 ACCESSION  
 U80924  
 VERSION  
 U80924.1 GI:1773032  
 KEYWORDS  
 SEGMENT  
 SOURCE  
 ORGANISM  
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 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS  
 Wong J.M., Myers, S.J., Tsou, C.L., Gosling, J., Arai, H. and  
 Charo, I.F.  
 TITLE  
 Organization and differential expression of the human monocyte  
 chemoattractant protein 1 receptor gene. Evidence for the role of  
 the carboxyl-terminal tail in receptor trafficking  
 J. Biol. Chem. 272 (2), 1038-1045 (1997)  
 JOURNAL  
 MEDLINE  
 PUBMED  
 97150864  
 8995400  
 2 (bases 1 to 5471)  
 REFERENCE  
 AUTHORS  
 Myers, S.J. and Charo, I.F.  
 TITLE  
 Direct Submission  
 JOURNAL  
 Submitted (04-DEC-1996) Pharmacology, Emory University, 1510  
 Clifton Road, Atlanta 30322, USA  
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Genbank accession number U80924, two alternatively spliced mRNAs."

Genbank accession number U80924, two alternatively spliced mRNAs."





QY	1219	TGTGATTCACAGTGAATCTTGGTGTCTACGTTACCAAGCAGGAAGGCTGAGAGGAG	1278
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QY	1339	AATACAGGATAGAGTTCAGACTTTTAAATAGTAAAAATAAAATTAAGCTGAAAC <td>1398</td>	1398
QY	1399	TGCAACTGTAAATGGTAAAGAGTTAGTTTGCATGCTATCATGTCAAAACGTAAGAT <td>1458</td>	1458
QY	1459	GCTGATATAGTACAGAGATAATCTTACGCTTGAAGTAAAGATTTTGAAGCTGAAAT <td>1518</td>	1518
QY	1519	GTTGGGAGACTGCTGAGTCAACCCCAATAGTTTGTGATGGCAGGAGTTGGAGTGTGTG <td>1578</td>	1578
QY	1579	ATCTGTGGGACATTAACCTATGTCATGTCAGTCAATCTCTCAGGCTTGCATGCA <td>1638</td>	1638
QY	1639	CAGTATAGCTCCATCCTGCTCATCTCAGTGGATCTCCATCTCTCAGGCTTGCATGCA <td>1698</td>	1698
QY	1699	AAAGCCTTTTGTGTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATG <td>1758</td>	1758
QY	1759	GTTCAGTGCCTCCAGATGCTTGTATGCTATGCTATGCTATGCTATGCTATGCTATGCT <td>1818</td>	1818
QY	1819	CTCCTAAATCAAAATGGCTTCTAATCAAAAGCTTTTAAACCCCTATGTTAAAGATGGA <td>1878</td>	1878
QY	1879	GTGGAGAGCTCCCTGAGTGAAGCAAGACATCTCTTGTAGTCGAGCAAGTTAAAGATG <td>1938</td>	1938
QY	1939	TTCTTATGTTGCCAGTGTGTTCTGATCTGATGCAAGCAAGCAAGCAAGCAAGCAAG <td>1998</td>	1998
QY	1999	ACAGGCACTTGGAGATAGACTCCCAAGCTGGAGTATGCTCTACTTTTCAGGCCACAT <td>2058</td>	2058
QY	2059	GGCTAAAGAGTTTCAGAAAAAGTGGGGACAGCAGACAGACTTTCACCTTCATATATT <td>2118</td>	2118
QY	2119	GTATGATTCCTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG <td>2178</td>	2178
QY	2179	TTTAAACAACTATGATTTGGAAAAATAAATCAATGCTATACTATGTTGATAAAAG <td>2238</td>	2238
QY	2239	TTTAAACAACTATGATTTGGAAAAATAAATCAATGCTATACTATGTTGATAAAAG <td>2298</td>	2298

AC098613

AC098613.2 GI:22038607

HTG.

human.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.

Direct Submission

Unpublished

2 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Raymond, C. and Haugen, E.D.

Direct Submission

Submitted (26-Oct-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

3 (bases 1 to 185437)

Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Saenphimmachak, C., Phelps, K.A., Buckley, D., Kibukawa, M., Raymond, C. and Haugen, E.D.

Direct Submission

Submitted (01-AUG-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA

On Aug 1, 2002 this sequence version replaced gi:16445164.

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Center: University of Washington Genome Center

Center Code: UWGC

Web site: <http://www.genome.washington.edu>

Contact: [uwgctg@u.washington.edu](mailto:uwgctg@u.washington.edu)

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Project Information

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Center project name: chr-3

Center clone name: RP11-24F11 (bc0137)

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Summary Statistics

Sequencing vector: plasmid; L08752; 100% of reads

Chemistry: Dye-terminator ET; 93% of reads

Chemistry: Dye-terminator Big Dye; 7% of reads

Assembly program: Phrap; version 0.990319

Consensus quality: 184860 bases at least Q40

Consensus quality: 185398 bases at least Q30

Consensus quality: 185435 bases at least Q20

Insert size: 185437; sum-of-contigs

Quality coverage: 7.6x in Q20 bases; sum-of-contigs

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Overlapping Sequences:

5': BAC-110P12 U95626, 111014-bp overlap

3': RP11-509121 (UWGC:bc0454) AC104304, 61294-bp overlap

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Sequence Quality Assessment:

This entry has been annotated with sequence quality estimates computed by the Phrap assembly program.

All manually edited bases have been reduced to quality zero.

Quality levels above 40 are expected to have less than 1 error in 10,000 bp.

Base-by-base quality values are not generally visible from the GenBank flat file format but are available as part of this entry's ASN.1 file.

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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., Phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

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Sequence Validation:

This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC

AC098613

AC098613.2

185437 bp

DNA

linear

PRI 01-AUG-2002

LOCUS

Human chromosome 3 clone RP11-24F11, complete sequence.

RESULT 7	185437 bp	DNA	linear	PRI 01-AUG-2002
AC098613				
LOCUS	AC098613			
DEFINITION	Homo sapiens chromosome 3 clone RP11-24F11, complete sequence.			



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Db	16444	TGTGATTCACAGTGTGAATCTTGCTGCTACGTTACAGGCAGGAAGGCTGAGAGGAG	16503
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QY	1339	AATACAGCATAGAGTTTCAGACTTTTAAATAGTAAATAAATAAATAAAGCTGAAAC	1398
Db	16564	AATACAGCATAGAGTTTCAGACTTTTAAATAGTAAATAAATAAATAAAGCTGAAAC	16623
QY	1399	TGCAACTTGTAAATGTGTAAGAGTATTTAGTTGCTATCATGTCACAACTGCAAAAT	1458
Db	16624	TGCAACTTGTAAATGTGTAAGAGTATTTAGTTGCTATCATGTCACAACTGCAAAAT	16683
QY	1459	GCTGATTTAGTACACAGATATTTCTAGCTTTGAGCTTAAAGATTTTTCAGAGGTTAT	1518
Db	16684	GCTGATTTAGTACACAGATATTTCTAGCTTTGAGCTTAAAGATTTTTCAGAGGTTAT	16743
QY	1519	GTTCGGAGACTGCTGAGTCAACCAATAGTTGTTGATGGCAGAGTTGGAAGTGTG	1578
Db	16744	GTTCGGAGACTGCTGAGTCAACCAATAGTTGTTGATGGCAGAGTTGGAAGTGTG	16803
QY	1579	ATCTGTGGCACATTAGCCTATGTGCATGCAGCATCTAAGTAAATGATGCTGTTGAATCA	1638
Db	16804	ATCTGTGGCACATTAGCCTATGTGCATGCAGCATCTAAGTAAATGATGCTGTTGAATCA	16863
QY	1639	CAGTATACGCTCCATCGCTGCATCTCAGCTGATCTCCATCTCTCAGGCTTGCTGCCA	1698
Db	16864	CAGTATACGCTCCATCGCTGCATCTCAGCTGATCTCCATCTCTCAGGCTTGCTGCCA	16923
QY	1699	AAAGCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	1758
Db	16924	AAAGCCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	16983
QY	1759	GTTCAGTGTGGCAGATGCTCTGATGCTCATATTTGTTCCCTAATTTGCCAGTGGAA	1818
Db	16984	GTTCAGTGTGGCAGATGCTCTGATGCTCATATTTGTTCCCTAATTTGCCAGTGGAA	17043
QY	1819	CTCCTAAATCAAAATGGCTTCTAATCAAAAGCTTTTAAACCTATTTGTAAGAAATGGAAG	1878
Db	17044	CTCCTAAATCAAAATGGCTTCTAATCAAAAGCTTTTAAACCTATTTGTAAGAAATGGAAG	17103
QY	1879	GTGGAAGCTCCCTGAAGTAAGAAAGATTTCTCTAGTGCAGCAAGTTAAGAAATG	1938
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QY	1939	TTCTTATGTTGCCAGTGTCTTCTGATCTGATGCAAGCAAGAACTGGCTTCTAGA	1998
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QY	1999	ACCAGGCAACTTGGGAAGTACACTCCCAAGCTGGACTATGGCTTACTTTCAGGCCACAT	2058
Db	17224	ACCAGGCAACTTGGGAAGTACACTCCCAAGCTGGACTATGGCTTACTTTCAGGCCACAT	17283
QY	2059	GGCTAAAGAGGTTTCAGAAAGAGTGGGACAGACAGACTTTCACCTTCATATATTT	2118
Db	17284	GGCTAAAGAGGTTTCAGAAAGAGTGGGACAGACAGACTTTCACCTTCATATATTT	17343
QY	2119	GTATGATCCTAATGAATGCATAAATGTTAAGTTGATGGTGTATGAAATGTAATCTGTT	2178
Db	17344	GTATGATCCTAATGAATGCATAAATGTTAAGTTGATGGTGTATGAAATGTAATCTGTT	17403
QY	2179	TTTAACTACTATGATTTGGAAATAAATCAATGCTATTAACATGTTGTAATAAG	2232
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RESULT	8		
G07239			
LOCUS		1068 bp	DNA
DEFINITION	human STS WI-9314, sequence tagged site.	linear	STS 19-OCT-1995

ACCESSION G07239.1 GI:860484

VERSION STS; STS sequence; primer; sequence tagged site.

KEYWORDS Homo sapiens STSs derived from sequences in dbEST and the Unigene collection.

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1068)

AUTHORS Hudson, T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically Mapped ESTs

JOURNAL Unpublished (1995)

COMMENT Contact: Thomas Hudson  
Whitehead Institute/MIT Center for Genome Research  
Whitehead Institute for Biomedical Research  
9 Cambridge Center, Cambridge MA 02142 USA  
Tel: 617 252 1900  
Fax: 617 252 1902  
Email: thudson@genome.wi.mit.edu

Primer A: GGAATCACAGCTCTGGCTT  
Primer B: ACTGTTTCCAAACCCAGCTG  
STS size: 114  
PCR Profile:  
  Presoak:  
    Denaturation:  
    Annealing: 56 degrees C  
    Polymerization:  
    PCR Cycles: 35  
    Thermal Cycler:  
Protocol:  
  Template: 10 ng  
  Primer: each 5 pM  
  dNTPs: each 4 mM  
  taq Polymerase: 0.025 units/ul  
  Total Vol: 20 ul

Buffer:  
  MgCl2: 1.5 mM  
  KCl: 50 mM  
  Tris-HCl: 10 mM  
  pH: 9.3

Prepared with primer pairs derived from U03882 -- Unigene.

FEATURES  
  source  
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      /organism="Homo sapiens"  
      /db\_xref="taxon:9606"  
      /map="730\_D\_5; 913\_C\_5; 941\_A\_7; 743\_H\_10; 781\_B\_10;  
      881\_F\_10; 881\_F\_11"

STS  
  primer\_bind 27..140  
  primer\_bind 27..46  
  primer\_bind complement(121..140) 329 t  
  BASE COUNT 315 a 186 c 238 g 329 t

ORIGIN  
  Query Match 47.8%; Score 1068; DB 11; Length 1068;  
  Best Local Similarity 100.0%; Pred. No. 2.7e-273;  
  Matches 1068; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1165 AGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTCTGCTTCACAGATGTGTGAT 1224  
  |||||  
  1 AGACAGAAATGACAGATCTCTGCTTTGGAAATCACACGCTCTGCTTCACAGATGTGTGAT 60

QY 1225 TCACAGTGTGAATCTTGTGCTAGCTTACCAGGAGGAAGGCTGAGAGGAGAGACTC 1284  
  |||||  
  61 TCACAGTGTGAATCTTGTGCTAGCTTACCAGGAGGAAGGCTGAGAGGAGAGACTC 120

QY 1285 CAGCTGGGTGGAAACAGTATTTTCCAACTACCTTCCAGTTCCTCATTTTGAATACA 1344  
  |||||  
  121 CAGCTGGGTGGAAACAGTATTTTCCAACTACCTTCCAGTTCCTCATTTTGAATACA 180

QY 1345 GCATAGAGTTCCAGACTTTTAAATAGTAAATAAATAAAGCTGAAACTGCAAC 1404  
Db 181 GCATAGAGTTCCAGACTTTTAAATAGTAAATAAATAAAGCTGAAACTGCAAC 240  
QY 1405 TTGTAATGTGGTAAAGAGTTAGTTGAGTTCCTATCATGTCAAAAGCTGAAATGCTGA 1464  
Db 241 TTGTAATGTGGTAAAGAGTTAGTTGAGTTCCTATCATGTCAAAAGCTGAAATGCTGA 300  
QY 1465 TTAGTCACAGAGTAATTTCTAGCTTTGAGCTTAAGAAATTTTCAGCAGGTGGTATGTTGG 1524  
Db 301 TTAGTCACAGAGTAATTTCTAGCTTTGAGCTTAAGAAATTTTCAGCAGGTGGTATGTTGG 360  
QY 1525 GAGACTGCTGAGTCAACCAATAGTTGTTGATGTCAGAGGTGGAAAGTGTGATCTGT 1584  
Db 361 GAGACTGCTGAGTCAACCAATAGTTGTTGATGTCAGAGGTGGAAAGTGTGATCTGT 420  
QY 1585 GGGCACATTAAGCTTATGTCATGAGCTATGATGTTGATGTTGATGTTGATGTTGATGTTGAT 1644  
Db 421 GGGCACATTAAGCTTATGTCATGAGCTATGATGTTGATGTTGATGTTGATGTTGATGTTGAT 480  
QY 1645 ACCTTCATGCTGTCATGTCAGCTGATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1704  
Db 481 ACCTTCATGCTGTCATGTCAGCTGATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 540  
QY 1705 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 1764  
Db 541 TTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGT 600  
QY 1765 GTCTTCGCGAGTGTCTGATGCTCATATTTGTTCCCTAATTTCCAGTGGAACTCCTA 1824  
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QY 1825 AATCAAAATGGCTTCTAATCAAAAGCTTTTAAACCTATTGGTAAAGAAATGGAAGTGGAG 1884  
Db 661 AATCAAAATGGCTTCTAATCAAAAGCTTTTAAACCTATTGGTAAAGAAATGGAAGTGGAG 720  
QY 1885 AGCTCCCTGAAGTAAGCAAGAACTTTCCCTTTAGTTCGAGCCCAAGTTAAGAAATGTTCTTA 1944  
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QY 1945 TGTTCGCCAGTGTGTTCTGATGCTGATGCAAGCAAGAAACACTGGGCTTCTAGAACCAGG 2004  
Db 781 TGTTCGCCAGTGTGTTCTGATGCTGATGCAAGCAAGAAACACTGGGCTTCTAGAACCAGG 840  
QY 2005 CAACTTGGGAAGTACACTCCCAAGCTGGACTATGGCTCTACTTTCAGGCCACATGGCTAA 2064  
Db 841 CAACTTGGGAAGTACACTCCCAAGCTGGACTATGGCTCTACTTTCAGGCCACATGGCTAA 900  
QY 2065 AGAAGGTTTCAGAAAGAGTGGGACAGAGCAAGAACTTTTACCTTCTATATATTTGATGA 2124  
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QY 2125 TCCTAATGAATGCATAAATGTTAGTTGATGCTGATGATGAATGTAATGTAATGTTTAACT 2184  
Db 961 TCCTAATGAATGCATAAATGTTAGTTGATGCTGATGATGAATGTAATGTAATGTTTAACT 1020  
QY 2185 AACTATGATTTGGAATAAATCAATGCTATAAATGATGTTGATGAATG 2232  
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RESULT 9  
ARL16075  
LOCUS  
DEFINITION Sequence 3 from patent US 6132987.  
ACCESSION ARL16075  
VERSION ARL16075.1  
KEYWORDS GI:14096397  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1979)  
PAT 16-MAY-2001

AUTHORS Charo, I. F. and Coughlin, S. R.  
TITLE Recombinant mammalian monocyte chemotactic protein-1 (MCP-1) receptors (MCP-1R, CCR-2)  
JOURNAL Patent: US 6132987-A 3 17-0CT-2000;  
FEATURES Location/Qualifiers  
source 1. .1979  
BASE COUNT 530 a 435 c 451 g 563 t  
ORIGIN

Query Match 43.9%; Score 980; DB 6; Length 1979;  
Best Local Similarity 100.0%; Pred. No. 7.9e-250;  
Matches 980; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATTGAACAGGACGCAATTTCCCCAGTACATCCACAACATGCTGTCACATCTCGTTCT 60  
Db 42 GGATTGAACAGGACGCAATTTCCCCAGTACATCCACAACATGCTGTCACATCTCGTTCT 101  
QY 61 CGGTTTTATCAGAATATCCAAAGAGAGGGGTGAAGAAGTCAACCTTTTTGATTATGAT 120  
Db 102 CGGTTTTATCAGAATATCCAAAGAGAGGGGTGAAGAAGTCAACCTTTTTGATTATGAT 161  
QY 121 TACGGTCTCCCTGTCTATAAATTTGACGTGAAGCAAAATGSGGCCCAACTCCTGCCCTCG 180  
Db 162 TACGGTCTCCCTGTCTATAAATTTGACGTGAAGCAAAATGSGGCCCAACTCCTGCCCTCG 221  
QY 181 CTCCTACTCGCTGGTTCATCTTTTGGTGGTGGCAACATGCTGGTCTGCTCATCTTA 240  
Db 222 CTCCTACTCGCTGGTTCATCTTTTGGTGGTGGCAACATGCTGGTCTGCTCATCTTA 281  
QY 241 ATAAACTGCAAAAGCTGAAGTGTGACTGACATTTACCTGCTCAACCTGGCCATCTCT 300  
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QY 301 GATCTGCTTTTCTTATTACTCTCCATTTGGGCTCACTCTGCTGCAAAATGAGTGGTC 360  
Db 342 GATCTGCTTTTCTTATTACTCTCCATTTGGGCTCACTCTGCTGCAAAATGAGTGGTC 401  
QY 361 TTTGGGAATGCAATGTCGAAATTTATTCACAGGCTGTATACATCGGTTATTTGGCGGA 420  
Db 402 TTTGGGAATGCAATGTCGAAATTTATTCACAGGCTGTATACATCGGTTATTTGGCGGA 461  
QY 421 ATCTTCTTCATCTCTCTGACAAATCGATAGATACCTGGCTATTGCTCCATGCTGTTT 480  
Db 462 ATCTTCTTCATCTCTCTGACAAATCGATAGATACCTGGCTATTGCTCCATGCTGTTT 521  
QY 481 GCTTTAAAGCCAGGACGCTACCTTTGGGGTGGTGAAGAAGTGTGATCACTGGTGGTG 540  
Db 522 GCTTTAAAGCCAGGACGCTACCTTTGGGGTGGTGAAGAAGTGTGATCACTGGTGGTG 581  
QY 541 GCTGTGTTTGGCTTCTGTCGCCAGGAATCATCTTTACTAAATGCCAGAAAGATTTCTGTT 600  
Db 582 GCTGTGTTTGGCTTCTGTCGCCAGGAATCATCTTTACTAAATGCCAGAAAGATTTCTGTT 641  
QY 601 TATGCTGTGGCCCTTATTTTCCAGGAGTGAATTAATTTCCACACAATATGAGGAAC 660  
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QY 721 ACCCTGCTCGGTGTGAAACAGAGAGGAGGATAGGGCAGTGAGAGTCACTCTTACC 780  
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QY 781 ATCATGATTTTACTTCTCTCTGACTCCCTATTAACATTTGTCATTTCTCTCTCTCTCTCT 840  
Db 822 ATCATGATTTTACTTCTCTCTGACTCCCTATTAACATTTGTCATTTCTCTCTCTCTCTCT 881  
QY 841 TTCCAGGAATTTCTCGGCTGAGTAACTGTGAAAGCAGTCACTGAGGACCAAGCCACG 900  
Db 882 TTCCAGGAATTTCTCGGCTGAGTAACTGTGAAAGCAGTCACTGAGGACCAAGCCACG 941

QY	901	CAGGTGACAGAGACTTTGGGATGACCTGCTGCTGATCCATCCATCATCTATGCGCTTC	960
Db	942	CAGGTGACAGAGACTTTGGGATGACCTGCTGCTGATCCATCCATCATCTATGCGCTTC	1001
QY	961	GTTCGGGAGAGTTTCAGAAG	980
Db	1002	GTTCGGGAGAGTTTCAGAAG	1021
RESULT 10			
LOCUS	I79543	1979 bp	DNA linear PAT 10-JUN-1998
DEFINITION	Sequence 3 from patent US 5707815.		
ACCESSION	I79543		
VERSION	I79543.1	GI:3207833	
KEYWORDS	Unknown.		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 1979)		
AUTHORS	Charo,I.F. and Coughlin,S.R.		
TITLE	Mammalian monocyte chemoattractant protein receptors and assays using them		
JOURNAL	Patent: US 5707815-A 3 13-JAN-1998;		
FEATURES	Location/Qualifiers		
source	1..1979		
BASE COUNT	530 a 435 c 451 g 563 t		
ORIGIN			
Query Match	43.9%;	Score 980;	DB 6; Length 1979;
Best Local Similarity	100.0%;	Pred. No. 7.9e-250;	
Matches 980;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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QY	61	CGTTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTCAACACCTTTTGGATTATGAT	120
Db	102	CGTTTTATCAGAAATACCAACGAGAGCGGTGAAGAGTCAACACCTTTTGGATTATGAT	161
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Db	222	CTCTACTCGTGTGTTTCATCTTTTGTGGGCAACATGCTGGTGGTCCCTCATCTTA	281
QY	241	ATAACTGCAAAAGCTGAAGTGTGACGTGACATTTACCTGCTCAACCTGGCCATCTCT	300
Db	282	ATAACTGCAAAAGCTGAAGTGTGACGTGACATTTACCTGCTCAACCTGGCCATCTCT	341
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Db	342	GATCTGCTTTTCTTATCTCTCCCATTTGGGCTCACCTGCTGCTGCAAAATGAGTGGTC	401
QY	361	TTTGGGAATGCAATGTGCAAAATTTACAGAGGCTGTATACATCGGTTATTTTGGCGGA	420
Db	402	TTTGGGAATGCAATGTGCAAAATTTACAGAGGCTGTATACATCGGTTATTTTGGCGGA	461
QY	421	ATCTTCTTCATCATCTCTGTCGACAAATCGATAGATACCTGGCTATGTCATCGCTGTTT	480
Db	462	ATCTTCTTCATCATCTCTGTCGACAAATCGATAGATACCTGGCTATGTCATCGCTGTTT	521
QY	481	GCTTTAAAGCCAGACGGTCACCTTTGGGGTGGTGAACAGTGTGATCACCTGGTTGGTG	540
Db	522	GCTTTAAAGCCAGACGGTCACCTTTGGGGTGGTGAACAGTGTGATCACCTGGTTGGTG	581
QY	541	GCTGTGTTGCTTCTGTCGCCAGGAATCATCTTTTACTAAATGCCAGAAAGAGATTCTGTT	600
Db	582	GCTGTGTTGCTTCTGTCGCCAGGAATCATCTTTTACTAAATGCCAGAAAGAGATTCTGTT	641
QY	601	TATGCTGTGCGCCCTTATTTTCCAGGATGGATTAATTTCCACACAATATGAGGAAC	660
Db	642	TATGCTGTGCGCCCTTATTTTCCAGGATGGATTAATTTCCACACAATATGAGGAAC	701
QY	661	ATTTTGGGGCTGGTCTGCGCTGCTCATCTGTCATGTCATCTGCTACTCGGGAATCTTGAAA	720
Db	702	ATTTTGGGGCTGGTCTGCGCTGCTCATCTGTCATCTGCTACTCGGGAATCTTGAAA	761
QY	721	ACCTTGTCTTCGGTGTGCAAAAGAGAGAGGCAATAGGGCAGTGAAGTCACTCTTCACC	780
Db	762	ACCTTGTCTTCGGTGTGCAAAAGAGAGAGGCAATAGGGCAGTGAAGTCACTCTTCACC	821
QY	781	ATCATGATGTTTACTTCTTCTTGGACTCCCTATAACATTTGTCATTTCTCTCGACACC	840
Db	822	ATCATGATGTTTACTTCTTCTTGGACTCCCTATAACATTTGTCATTTCTCTCGACACC	881
QY	841	TTCCAGGAATTTCTCGGCTGAGTAACTGTGAAGCACCAGTCACTGGACCAAGCCAGC	900
Db	882	TTCCAGGAATTTCTCGGCTGAGTAACTGTGAAGCACCAGTCACTGGACCAAGCCAGC	941
QY	901	CAGGTGACAGACACTTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCTTTC	960
Db	942	CAGGTGACAGACACTTTGGGATGACTCACTGCTGCATCAATCCCATCATCTATGCTTTC	1001
QY	961	GTTCGGGAGAGTTTCAGAAG	980
Db	1002	GTTCGGGAGAGTTTCAGAAG	1021
RESULT 11			
LOCUS	HSU03905	1979 bp	mRNA linear PRI 22-JUN-1994
DEFINITION	Human monocyte chemoattractant protein 1 receptor (MCP-1RB)		
ACCESSION	U03905		
VERSION	U03905.1	GI:472557	
KEYWORDS	alternatively spliced mRNA, complete cds.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	1 (bases 1 to 1979)		
AUTHORS	Charo,I.F., Myers,S.J., Herman,A., Franci,C., Connolly,A.J. and Coughlin,S.R.		
TITLE	Molecular cloning and functional expression of two monocyte chemoattractant protein 1 receptors reveals alternative splicing of the carboxyl-terminal tails		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 91 (7), 2752-2756 (1994)		
MEDLINE	94195821		
PUBMED	8146186		
REFERENCE	2 (bases 1 to 1979)		
AUTHORS	Myers,S.J.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-DEC-1993) Scott J. Myers, Cardiovascular, The Gladstone Institutes, 2550 23rd Street, San Francisco, CA 94110, USA		
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Db	162	TACGGTGCCTCGCTCATAAATTTGACGTGAAGCAAAATGGGGCCCAACTCTCGCTCCG	221
QY	181	CTCTACTCGCTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCGTCTCATCTTA	240
Db	222	CTCTACTCGCTGGTGTTCATCTTTGGTTTGTGGGCAACATGCTGGTCGTCTCATCTTA	281
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Db	342	GATCTGCTTTTCTTATTACTCTCCCAATTTGGGCTCACTGCTGCAAAATGAGTGGTC	401
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QY	421	ATCTCTTCTCATCATCTCTCGTGAATCGATAGATACCTGGCTATGTGCCATGCTGTCTT	480
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QY	481	GCTTTAAAGCCAGGACGGTCACCTTTGGGGTGGTGACAAAGTGTGATCACTGCTGGTG	540
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VERSION	AX232506.1	GI:15592569	
KEYWORDS	human.		
SOURCE	human.		
ORGANISM	Homo sapiens		
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AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Valdes, A.M., Groot, P.H. and Spurr, N.K.		
JOURNAL	Ccr2-641, polymorphic variant of the human ccr2 receptor and its		
FEATURES	use in the diagnostic and treatment of atherosclerosis		
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DEFINITION	Human mRNA for monocyte chemoattractant protein 1 receptor (MCP-1 receptor), complete cds.		
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VERSION	D29984.1	GI:531246	
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SOURCE	Homo sapiens monocyte cell-line THP-1 cDNA to mRNA.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	Yamagami, S., Tokuda, Y., Ishii, K., Tanaka, H. and Endo, N.		
JOURNAL	cDNA cloning and functional expression of a human monocyte		
MEDLINE	chemoattractant protein 1 receptor		
REFERENCE	Biochem. Biophys. Res. Commun. 202 (2), 1156-1162 (1994)		
JOURNAL	94324942		
AUTHORS	2 (bases 1 to 1083)		
REFERENCE	Yamagami, S.		
JOURNAL	unpublished		
REFERENCE	3 (bases 1 to 1083)		

AUTHORS	Yamagami, S.
TITLE	Direct Submission
JOURNAL	Submitted (22-Apr-1994) Shinsuke Yamagami, TEIJIN LIMITED, Institute for Bio-Medical Research; 4-3-2 Asahigaoka, Hino, Tokyo 191, Japan (Tel:0423-86-8282)
COMMENT	Submitted (22-Apr-1994) to DDBJ by:

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Hino, Tokyo 191  
Japan  
Phone: 0425-86-8282  
Fax: 0425-87-5512

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255 a 259 c 247 g 322 t
BASE COUNT

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Best Local Similarity	99.9%				Pred. No. 5.1e-239;
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